REMARKS

Reconsideration of this Application is respectfully requested. Claims 11-14, 16-17, and 19 are pending. Claim 12 has been cancelled. Claim 11 has been amended to incorporate the limitations of claim 12. No new matter is added by way of these amendments as support for this amendment may be found throughout the specification and original claims, and as more specifically described below. Therefore, Applicants request that the amendments be entered.

Objections to the Specification

A. Amendment to reflect change in status of parent application.

The Examiner has requested that the claim for domestic priority in the first paragraph be amended to include the present status of the parent application, i.e., to include the issued U.S. Patent Number.

Applicants' Response:

Paragraph 1 on page 1, lines 4-5, of the present application has been amended to reflect the change in status to U.S. Patent Application No. 09/855,341.

B. Amendment to Correct Missing Sequence Identifiers

Rule 37 C.F.R. 1.821(d) requires use of the assigned sequence identifier (e.g. SEQ ID NO: X) in all instances where the description or claims of a patent application discuss sequences. Specifically, Figure 1 illustrates a sequence comparison between several sequences described in the specification. No sequence identifiers are included in Figure 1.

Applicants' Response:

The Applicants respectfully call to the attention of the Examiner the Manual of Patent Examining Procedure ("MPEP") section 2422.02 entitled "**The Requirement for**

Exclusive Conformance; Sequences Presented in Drawing Figures". MPEP 2422.02 states: "In view of the fact that many significant sequence characteristics may only be determined by a figure, the exclusive conformance requirement of this section may be relaxed for drawing figures." In particular, the similarity or homology between/among sequences can only be depicted in an effective manner in a drawing figure.

Figure 1 depicts an amino acid sequence alignment of 4 sequences. The Applicants acknowledge that 2 of the sequences depicted in Figure 1 were inadvertently not included in the original sequence listing. As such, the Applicants have chosen to submit an amended sequence listing (including a copy in computer readable form) to include the 2 additional sequences (referred to as SEQ ID NOs: 17 and 18).

MPEP 2422.02 further states

> "...when a sequence is presented in the drawing, regardless of the format or the manner of presentation of that sequence in the drawing, the sequence must still be included in the Sequence Listing and the sequence identifier ("SEQ ID NO:X") must be used, **either** in the drawing **or** in the Brief Description of the Drawings." [emphasis added].

As such, the Applicants assert that it is not necessary in view of MPEP 2422.02 to submit an amended set of Figures. The Applicants have elected to amend the specification to include the missing sequence identifiers within the Brief Description of the Drawings and Sequence Descriptions. The amendments to the specification begin on page 2 of the present office action response.

Substitute Sequence Listing Under 37 C.F.R. § 1.825

As per 37 C.F.R § 1.825, please replace the SEQUENCE LISTING beginning on page 18 and concluding on page 23 of the published application with the amended sequence listing (substitute copy) provided on the attached substitute sheets (beginning on page 11) which form parts of the present office action response. Accordingly, the present substitute paper copy of the sequence listing is also

accompanied by a substitute copy of the sequence listing in computer readable form in accordance with (§ 1.821(e)). The updated paper and computer readable versions of the Sequence Listing are the same and present no new matter. Support for the changes to the sequence listing can be found in Figure 1 and in paragraph [0029] of the published application. The format of the sequence listing has been updated from PatentIn 2.1 to PatentIn version 3.4 as the Applicants believe that PatentIn 2.1 is not compatible with PatentIn version 3.4.

Objections to the Claims

Claim 12 has been objected for reciting "for the" instead of "forth".

Applicants' Response:

Claim 12 has been cancelled. The limitations of claim 12 have been incorporated into claim 11. As such, the objectionable text has been removed. The Applicants believe that Claim 11 is now free of the prior art and presently allowable.

Claim Rejections:

35 U.S.C. §103

The Examiner has rejected Claims 11, 13-14 and 16 under 35 U.S.C. § 103(a) as being unpatentable over Heide *et al.* (1995, German Patent Number DE 4423022C1, USPTO English translation) in light of Pichersky *et al.* (1993, *PNAS* 83(11):3880-3884). Claims 12, 17, and 19 were not rejected and are deemed free of the prior art. Claim 19 is currently allowed.

The Examiner states that Heide *et al.* discloses an expression cassette comprising a nucleic acid encoding a chorismate pyruvate lyase, wherein the nucleic acid encodes a polypeptide sequence which exhibits 100% sequence identity to Applicants' SEQ ID NO: 4 wherein the nucleic acid sequence of Heide *et al* is operably linked to a nucleic acid sequence encoding a chloroplast transit peptide. Heide *et al.* disclose a tobacco transformed with said cassette and other plants that can be transformed by said cassette. Heide *et al* does not teach a nucleic acid encoding the amino acid sequence of SEQ ID NO: 15, wherein said sequence is operably linked to SEQ ID NO: 4, wherein SEQ ID NO: 4 encodes a CPL protein.

The Examiner believes that Pichersky *et al.* teaches a nucleic acid sequence encoding a chloroplast transit peptide that exhibits 97% amino acid identity to SEQ ID NO: 15. The Examiner further states in the present office action:

> "The Office contends that the sequence of Pichersky *et al.* would actually encoded (sic) a transit peptide exhibiting 100% identity with Applicants' SEQ ID NO: 15 because the sequence of Pichersky *et al.* encoding an amino acid sequence that is only one amino acid shorter than Applicants' SEQ ID NO: 15. Given that Pichersky *et al.* cite articles disclosing nucleic acids encoding the small subunit of the ribulose-bisphosphate carboxylase gene and given that Pichersky *et al.* themselves disclose nucleic acid sequences encoding the small subunit of the ribulose-bisphosphate carboxylase gene from tomato, **the Office contends that the one amino acid difference is due to an annotation error**. Therefore, the Office considers the sequence of Pichersky *et al.* to encode Applicants' SEQ ID NO: 15 absent evidence to the contrary." [bold emphasis added]

Applicants' Response:

The Applicants respectfully disagree. The Applicants agree with the Examiner that Heide *et al.* does not teach a nucleic acid molecule encoding the protein of SEQ ID NO: 15. Furthermore, the Applicants strongly disagree with the Examiner's position that Pichersky *et al.* teaches SEQ ID NO:15 and that the difference is the result of a purely hypothetical annotation error.

Pichersky *et al.* discloses the protein sequence for 3 different ribulose-1,5-bisphosphate carboxylase subunits from tomato (RBSC-1, RBSC-2A, and RBSC-3A) and a single sequence from tobacco (see Figure 4, page 3883 of Pichersky *et al.*). Pichersky *et al.* illustrates the natural transit peptide sequence for each, including the natural cleavage site. None of the sequences in Pichersky *et al.* match Applicants' SEQ ID NO: 15 transit peptide sequence, which includes a transit peptide donor sequence (See Figure 1 of the present application). Furthermore, each of the sequences provided in Pichersky *et al.* (RBSC-1, RBSC-2A, and RBSC-3A) were deposited by E. Pichersky to GenBank® under Accession Numbers AAA34188, AAA34189, and AAA341190; respectively on October 31, 1986. The only reference

cited in each of these GenBank® entries was Pichersky *et al.* (*PNAS*, 83(11):3880-3884 (1986); the reference currently being cited by the Examiner in the present rejection.

A Clustal W alignment of the Applicants transit peptide ("SEQ_15" representing SEQ ID NO: 15) versus the sequences for RBSC-1 (AAA34188.1), RBSC-2A (AAA34189.1), and RBSC-3A (AAA341190.1) is provided below. The arrow indicates the transit peptide cleavage site. The underlined portion indicates the transit peptide donor sequence (a modified 5 amino acid sequence derived from, but different to, the mature form of the rubulose-1,5-bisphosphate carboxylase sequence) fused to the chorismate pyruvate lyase (CPL) after post-translational processing. The unique histidine residue within the transit peptide donor sequence is bolded.

CLUSTAL W multiple sequence alignment

```
                                                                    ↓
AAA34190.1 MASSVMSSAAVATRGNGAQASMVAPFTGLKSTASFPVSRKQN-LDITSIASNGGRVSCMQ
AAA34188.1 MASSIVSSAAAATRSNVAQASMVAPFTGLKSAASFPVTKKNNNVDITSLASNGGRVRCMQ
SEQ_15     MASSVISSAAVATRSNVTQASMVAPFTGLKSSATFPVTKKQN-LDITSIASNGGRVSCMQ
AAA34189.1 MASSVISSAAVATRSNVTQASMVAPFTGLKSSATFPVTKKQN-LDITSIASNGGRVSCMQ
           ****::****.***.*::**************:*:***::*:* :****:******* ***

AAA34190.1 VWPPINMKKYETLSYLPDLSDEQLLSEIEYLLKNGWVPCLEFETEHGFVYRENHKSPGYY
AAA34188.1 VWPPINMKKYETLSYLPDLSDEQLLSEIEYLLKNGWVPCLEFETERGFVYRENNSSPGYY
SEQ_15     VWH-------------------------------------------------------
AAA34189.1 VWPPINMKKYETLSYLPDLSDEQLLSEIEYLLKNGWVPCLEFETEHGFVYRENNKSPGYY
           **

AAA34190.1 DGRYWTMWKLPMFGCTDATQVLAEVQEAKKAYPQAWVRIIGFDNVRQVQCISFIAYKPEG
AAA34188.1 DGRYWTMWKLPMFGCTDATQVLAEVQEAKKAYPQAWVRIIGFDNVRQVQCISFIAYKPEG
SEQ_15     ------------------------------------------------------------
AAA34189.1 DGRYWTMWKLPMFGCTDATQVLAEVQEAKKAYPQAWVRIIGFDNVRQVQCISFIAYKPEG

AAA34190.1  Y
AAA34188.1  F
SEQ_15      -
AAA34189.1  Y
```

Clearly, Pichersky *et al.* does not teach SEQ ID NO: 15 nor is this difference a hypothetical annotation error as suggested by the Examiner. The unique chloroplast-targeting sequence as represented by SEQ ID NO: 15 is not taught by Heide *et al.* or Pichersky *et al.*

In order to form a valid 35 U.S.C. 103(a), all of the limitations within the rejected claim must be found in the combination of references. Neither of the cited references teaches the chloroplast-targeting sequence as represented by SEQ ID

NO: 15. As such, the Applicants respectfully request withdrawal of this rejection and allowance of Claim 16.

CONCLUSION

In view of the foregoing, Applicants respectfully request that the Examiner reconsider all presently outstanding objections and rejections and that they be withdrawn. Applicants believe that a full and complete reply has been made to the outstanding Office Action and, as such, the present application is in condition for allowance. The Applicants believe that the present claim amendments and remarks are proper in response to final rejection and should be admitted. Therefore, allowance of the above-referenced application is respectfully requested.

If the Examiner believes, for any reason, that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Respectfully submitted,

Christine M. Lhulier

Christine M. Lhulier
ATTORNEY FOR APPLICANTS
REGISTRATION NO. 54,269
TELEPHONE: 302-992-5463
FACSIMILE: 302-992-5374

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